

1 ATGAGTGGCCTGGGCCGAGCAGGCGAGGTGGCCGAGCCGTGTGGACCAAGGAGGAGCGC 60  
1 M S G L G R S R R G G R S R V D Q E E R 20  
61 TTCCACAGGGCCTGTGGACGGGGGTGGCTATGAGATCCTGCCCGAAGAGCAGTACTGG 120  
21 F P Q G L W T G V A M R S C P E E Q Y W 40  
121 GATCCTCTGTGGGTACCTGCATGTCTGCAAAACCATTTGCAACCATCAGAGCCAGCGC 180  
41 D P L L G T C M S C K T I C N H Q S Q R 60  
181 ACCTGTGCAGCCTTCTGCAGGTCACTCAGCTGCCGCAAGGAGCAAGGCAAGTTCTATGAC 240  
61 T C A A F C R S L S C R K E Q G K F Y D 80  
241 CATCTCCTGAGGGACTGCATCAGCTGTGCTCCATCTGTGGACAGCACCCCTAAGCAATGT 300  
81 H L L R D C I S C A S I C G Q H P K Q C 100  
301 GCATACTTCTGTGAGAACAGCTCAGGAGCCAGTGAACCTTCCACCAGAGCTCAGGAGA 360  
101 A Y F C E N K L R S P V N L P P E L R R 120  
361 CAGCGGAGTGGAGAAGTTGAAAAACAATTGAGACCACTCGGGAAGGTACCAAGGATTGGAG 420  
121 Q R S G E V E N N S D N S G R Y Q G L E 140  
421 CACAGAGGCTCAGAAGCAAGTCCAGCTCTCCCGGGGCTGAAGCTGAGTGCAGATCAGGTG 480  
141 H R G S E A S P A L P G L K L S A D Q V 160  
481 GCCCTGGTCTACAGCACGCTGGGGCTCTGCCTGTGTGCCGTCTCTGTCTCTCTGGTG 540  
161 A L V Y S T L G L C L C A V L C C F L V 180  
541 GGGTGGCTGCTTCTCTCAAGAAGAGGGGGATCCCTGTCTCTGCCAGCCCCGCTCAAGG 600  
181 A V A C F L K K R G D P C S C Q P R S R 200  
601 CCCCGTCAAAGTCCGGCCAAGTCTTCCAGGATCACGCGATGGAAGCCGCGAGCCCTGTG 660  
201 P R Q S P A K S S Q D H A M E A G S P V 220  
661 AGCACAATCCCGAGCCAGTGGAGACCTGCAGCTTCTGCTTCCCTGAGTGCAGGGGCGCC 720  
221 S T S P E P V E T C S F C F P E C R A P 240  
721 ACGCAGGAGAGCGCAGTCAAGCCTGGGACCCCGACCCCACTTGTGCTGGAAGGTGGGGG 780  
241 T Q E S A V T P G T P D P T C A G R W G 260  
781 TGCCACACCAAGACCAAGTCTGCAAGCTTGCCACACATCCCAAGACAGTGGCCTTGGC 840  
261 C H T R T T V L Q P C P H I P D S G L G 280  
841 ATTGTGTGTGCTGCTGCCAGGAGGGGGGCCAGTGCATAA 882  
281 I V C V P A Q E G G P G A \* 294

**FIG. 1**

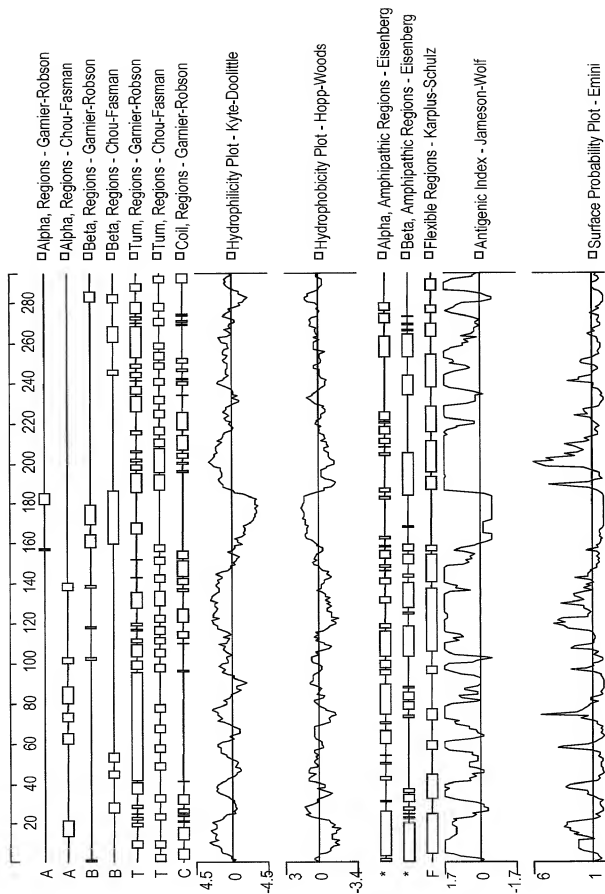


FIG. 2